

## SEQUENCE LISTING

<110> Novartis AG

<120> Organic Compound

<130> 4-32761P1/UNZ

<160> 44

<170> PatentIn version 3.1

<210> 1

<211> 18

<212> PRT

<213> Rattus norvegicus

<220>

<221> PEPTIDE

<222> (1)..(18)

<223> rat NogoA\_623-640

<400> 1

Ser Tyr Asp Ser Ile Lys Leu Glu Pro Glu Asn Pro Pro Pro Tyr Glu  
1 5 10 15

Glu Ala

<210> 2

<211> 221

<212> PRT

<213> Mus musculus

<220>

<221> CHAIN

<222> (1)..(221)

<223> Variable part of Heavy Chain of 11C7 with leader sequence

<400> 2

Met Asp Phe Gly Leu Ile Phe Phe Ile Val Gly Leu Leu Lys Gly Val  
1 5 10 15

Gln Cys Glu Val Lys Leu Leu Glu Ser Gly Gly Leu Val Gln Pro  
20 25 30

Gly Gly Ser Leu Lys Leu Ser Cys Val Val Ser Gly Phe Asp Phe Arg  
35 40 45

Arg Asn Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu  
50 55 60

Trp Ile Gly Glu Ile Asn Pro Asp Ser Ser Lys Ile Asn Tyr Thr Pro  
65 70 75 80

Ser Leu Lys Asp Lys Phe Ile Ile Ser Arg Asp Asn Ala Lys Asn Thr  
85 90 95

Leu Tyr Leu Gln Val Ser Thr Val Arg Ser Glu Asp Thr Ala Leu Tyr  
100 105 110

Tyr Cys Val Arg Pro Val Trp Met Tyr Ala Met Asp Tyr Trp Gly Gln  
115 120 125

Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val

130

135

140

Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr  
145 150 155 160

Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Thr  
165 170 175

Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val  
180 185 190

Leu Gln Ser Asp Leu Tyr Thr Leu Ser Ser Ser Val Thr Val Pro Ser  
195 200 205

Ser Thr Trp Pro Ser Glu Thr Val Thr Cys Asn Val Ala  
210 215 220

<210> 3

<211> 238

<212> PRT

<213> *Mus musculus*

<220>

<221> CHAIN

<222> (1) .. (238)

<223> Light Chain of 11C7 with leader sequence

<400> 3

Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu Trp Ile Arg Glu  
1 5 10 15

Thr Ser Gly Asp Val Leu Leu Thr Gln Thr Pro Leu Thr Leu Ser Ile  
20 25 30

Thr Ile Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu  
35 40 45

Leu His Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg Pro  
50 55 60

Gly Gln Ser Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser  
65 70 75 80

Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr  
85 90 95

Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Leu Tyr Tyr Cys  
100 105 110

Trp Gln Gly Thr His Phe Pro Gln Thr Phe Gly Gly Thr Lys Leu

115

120

125

Glu Ile Lys Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro  
130 135 140

Ser Ser Glu Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu  
145 150 155 160

Asn Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly  
165 170 175

Ser Glu Arg Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser  
180 185 190

Lys Asp Ser Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp  
195 200 205

Glu Tyr Glu Arg His Asn Ser Tyr Thr Cys Glu Ala Thr His Lys Thr  
210 215 220

Ser Thr Ser Pro Ile Val Lys Ser Phe Asn Arg Gly Glu Cys  
225 230 235

<210> 4

<211> 3919

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) .. (3579)

<223> Human NogoA

<400> 4

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Met Glu Asp Leu Asp Gln Ser Pro Leu Val Ser Ser Ser Asp Ser Pro  
1 5 10 15

ccc cgg ccg cag ccc gcg ttc aag tac cag ttc gtg agg gag ccc gag 96  
Pro Arg Pro Gln Pro Ala Phe Lys Tyr Gln Phe Val Arg Glu Pro Glu  
20 25 30

gac gag gag gaa gaa gag gag gag gaa gag gag gac gag gac gaa gac 144  
Asp Glu Glu Glu Glu Glu Glu Glu Glu Asp Glu Asp Glu Asp  
35 40 45

ctg gag gag ctg gag gtg ctg gag agg aag ccc gcc ggc ggg ctg tcc 192  
Leu Glu Glu Leu Glu Val Leu Glu Arg Lys Pro Ala Ala Gly Leu Ser  
50 55 60

gcg gcc cca gtg ccc acc gcc cct gcc ggc gcg ccc ctg atg gac 240  
Ala Ala Pro Val Pro Thr Ala Pro Ala Ala Gly Ala Pro Leu Met Asp  
65 70 75 80

ttc gga aat gac ttc gtg ccg ccg gcg ccc cgg gga ccc ctg ccg gcc 288  
Phe Gly Asn Asp Phe Val Pro Pro Ala Pro Arg Gly Pro Leu Pro Ala

85	90	95	
gct ccc ccc gtc gcc ccg gag cgg cag ccg tct tgg gac ccg agc ccg			336
Ala Pro Pro Val Ala Pro Glu Arg Gln Pro Ser Trp Asp Pro Ser Pro			
100	105	110	
gtg tcg tcg acc gtg ccc gcg cca tcc ccg ctg tct gct gcc gca gtc			384
Val Ser Ser Thr Val Pro Ala Pro Ser Pro Leu Ser Ala Ala Ala Val			
115	120	125	
tcg ccc tcc aag ctc cct gag gac gac gag cct ccg gcc cgg cct ccc			432
Ser Pro Ser Lys Leu Pro Glu Asp Asp Glu Pro Pro Ala Arg Pro Pro			
130	135	140	
cct cct ccc ccg gcc agc gtg agc ccc cag gca gag ccc gtg tgg acc			480
Pro Pro Pro Pro Ala Ser Val Ser Pro Gln Ala Glu Pro Val Trp Thr			
145	150	155	160
ccg cca gcc ccg gct ccc gcc ccg ccc tcc acc ccg gcc gcg ccc			528
Pro Pro Ala Pro Ala Ala Pro Pro Ser Thr Pro Ala Ala Pro			
165	170	175	
aag cgc agg ggc tcc tcg ggc tca gtg gat gag acc ctt ttt gct ctt			576
Lys Arg Arg Gly Ser Ser Gly Ser Val Asp Glu Thr Leu Phe Ala Leu			
180	185	190	
cct gct gca tct gag cct gtg ata cgc tcc tct gca gaa aat atg gac			624
Pro Ala Ala Ser Glu Pro Val Ile Arg Ser Ser Ala Glu Asn Met Asp			
195	200	205	
ttg aag gag cag cca ggt aac act att tcg gct ggt caa gag gat ttc			672
Leu Lys Glu Gln Pro Gly Asn Thr Ile Ser Ala Gly Gln Glu Asp Phe			
210	215	220	
cca tct gtc ctg ctt gaa act gct gct tct ctt cct tct ctg tct cct			720
Pro Ser Val Leu Leu Glu Thr Ala Ala Ser Leu Pro Ser Leu Ser Pro			
225	230	235	240

ctc tca gcc gct tct ttc aaa gaa cat gaa tac ctt ggt aat ttg tca	768		
Leu Ser Ala Ala Ser Phe Lys Glu His Glu Tyr Leu Gly Asn Leu Ser			
245	250	255	
aca gta tta ccc act gaa gga aca ctt caa gaa aat gtc agt gaa gct	816		
Thr Val Leu Pro Thr Glu Gly Thr Leu Gln Glu Asn Val Ser Glu Ala			
260	265	270	
tct aaa gag gtc tca gag aag gca aaa act cta ctc ata gat aga gat	864		
Ser Lys Glu Val Ser Glu Lys Ala Lys Thr Leu Leu Ile Asp Arg Asp			
275	280	285	
tta aca gag ttt tca gaa tta gaa tac tca gaa atg gga tca tcg ttc	912		
Leu Thr Glu Phe Ser Glu Leu Glu Tyr Ser Glu Met Gly Ser Ser Phe			
290	295	300	
agt gtc tct cca aaa gca gaa tct gcc gta ata gta gca aat cct agg	960		
Ser Val Ser Pro Lys Ala Glu Ser Ala Val Ile Val Ala Asn Pro Arg			
305	310	315	320
gaa gaa ata atc gtg aaa aat aaa gat gaa gaa gag aag tta gtt agt	1008		
Glu Glu Ile Ile Val Lys Asn Lys Asp Glu Glu Glu Lys Leu Val Ser			
325	330	335	
aat aac atc ctt cat aat caa caa gag tta cct aca gct ctt act aaa	1056		
Asn Asn Ile Leu His Asn Gln Gln Glu Leu Pro Thr Ala Leu Thr Lys			
340	345	350	
ttg gtt aaa gag gat gaa gtt gtg tct tca gaa aaa gca aaa gac agt	1104		
Leu Val Lys Glu Asp Glu Val Val Ser Ser Glu Lys Ala Lys Asp Ser			
355	360	365	
ttt aat gaa aag aga gtt gca gtg gaa gct cct atg agg gag gaa tat	1152		
Phe Asn Glu Lys Arg Val Ala Val Glu Ala Pro Met Arg Glu Glu Tyr			
370	375	380	

gca gac ttc aaa cca ttt gag cga gta tgg gaa gtg aaa gat agt aag 1200  
Ala Asp Phe Lys Pro Phe Glu Arg Val Trp Glu Val Lys Asp Ser Lys  
385 390 395 400

gaa gat agt gat atg ttg gct gct gga ggt aaa atc gag agc aac ttg 1248  
Glu Asp Ser Asp Met Leu Ala Ala Gly Gly Lys Ile Glu Ser Asn Leu  
405 410 415

gaa agt aaa gtg gat aaa aaa tgt ttt gca gat agc ctt gag caa act 1296  
Glu Ser Lys Val Asp Lys Lys Cys Phe Ala Asp Ser Leu Glu Gln Thr  
420 425 430

aat cac gaa aaa gat agt gag agt agt aat gat gat act tct ttc ccc 1344  
Asn His Glu Lys Asp Ser Glu Ser Ser Asn Asp Asp Thr Ser Phe Pro  
435 440 445

agt acg cca gaa ggt ata aag gat cgt tca gga gca tat atc aca tgt 1392  
Ser Thr Pro Glu Gly Ile Lys Asp Arg Ser Gly Ala Tyr Ile Thr Cys  
450 455 460

gct ccc ttt aac cca gca gca act gag agc att gca aca aac att ttt 1440  
Ala Pro Phe Asn Pro Ala Ala Thr Glu Ser Ile Ala Thr Asn Ile Phe  
465 470 475 480

cct ttg tta gga gat cct act tca gaa aat aag acc gat gaa aaa aaa 1488  
Pro Leu Leu Gly Asp Pro Thr Ser Glu Asn Lys Thr Asp Glu Lys Lys  
485 490 495

ata gaa gaa aag aag gcc caa ata gta aca gag aag aat act agc acc 1536  
Ile Glu Glu Lys Lys Ala Gln Ile Val Thr Glu Lys Asn Thr Ser Thr  
500 505 510

aaa aca tca aac cct ttt ctt gta gca gca cag gat tct gag aca gat 1584  
Lys Thr Ser Asn Pro Phe Leu Val Ala Ala Gln Asp Ser Glu Thr Asp  
515 520 525

tat gtc aca aca gat aat tta aca aag gtg act gag gaa gtc gtg gca 1632

Tyr Val Thr Thr Asp Asn Leu Thr Lys Val Thr Glu Glu Val Val Ala  
530 535 540

aac atg cct gaa ggc ctg act cca gat tta gta cag gaa gca tgt gaa 1680  
Asn Met Pro Glu Gly Leu Thr Pro Asp Leu Val Gln Glu Ala Cys Glu  
545 550 555 560

agt gaa ttg aat gaa gtt act ggt aca aag att gct tat gaa aca aaa 1728  
Ser Glu Leu Asn Glu Val Thr Gly Thr Lys Ile Ala Tyr Glu Thr Lys  
565 570 575

atg gac ttg gtt caa aca tca gaa gtt atg caa gag tca ctc tat cct 1776  
Met Asp Leu Val Gln Thr Ser Glu Val Met Gln Glu Ser Leu Tyr Pro  
580 585 590

gca gca cag ctt tgc cca tca ttt gaa gag tca gaa gct act cct tca 1824  
Ala Ala Gln Leu Cys Pro Ser Phe Glu Glu Ser Glu Ala Thr Pro Ser  
595 600 605

cca gtt ttg cct gac att gtt atg gaa gca cca ttg aat tct gca gtt 1872  
Pro Val Leu Pro Asp Ile Val Met Glu Ala Pro Leu Asn Ser Ala Val  
610 615 620

cct agt gct ggt gct tcc gtg ata cag ccc agc tca tca cca tta gaa 1920  
Pro Ser Ala Gly Ala Ser Val Ile Gln Pro Ser Ser Ser Pro Leu Glu  
625 630 635 640

gct tct tca gtt aat tat gaa agc ata aaa cat gag cct gaa aac ccc 1968  
Ala Ser Ser Val Asn Tyr Glu Ser Ile Lys His Glu Pro Glu Asn Pro  
645 650 655

cca cca tat gaa gag gcc atg agt gta tca cta aaa aaa gta tca gga 2016  
Pro Pro Tyr Glu Glu Ala Met Ser Val Ser Leu Lys Lys Val Ser Gly  
660 665 670

ata aag gaa gaa att aaa gag cct gaa aat att aat gca gct ctt caa 2064  
Ile Lys Glu Glu Ile Lys Glu Pro Glu Asn Ile Asn Ala Ala Leu Gln

675	680	685	
gaa aca gaa gct cct tat ata tct att gca tgt gat tta att aaa gaa			2112
Glu Thr Glu Ala Pro Tyr Ile Ser Ile Ala Cys Asp Leu Ile Lys Glu			
690	695	700	
aca aag ctt tct gct gaa cca gct ccg gat ttc tct gat tat tca gaa			2160
Thr Lys Leu Ser Ala Glu Pro Ala Pro Asp Phe Ser Asp Tyr Ser Glu			
705	710	715	720
atg gca aaa gtt gaa cag cca gtg cct gat cat tct gag cta gtt gaa			2208
Met Ala Lys Val Glu Gln Pro Val Pro Asp His Ser Glu Leu Val Glu			
725	730	735	
gat tcc tca cct gat tct gaa cca gtt gac tta ttt agt gat gat tca			2256
Asp Ser Ser Pro Asp Ser Glu Pro Val Asp Leu Phe Ser Asp Asp Ser			
740	745	750	
ata cct gac gtt cca caa aaa caa gat gaa act gtg atg ctt gtg aaa			2304
Ile Pro Asp Val Pro Gln Lys Gln Asp Glu Thr Val Met Leu Val Lys			
755	760	765	
gaa agt ctc act gag act tca ttt gag tca atg ata gaa tat gaa aat			2352
Glu Ser Leu Thr Glu Thr Ser Phe Glu Ser Met Ile Glu Tyr Glu Asn			
770	775	780	
aag gaa aaa ctc agt gct ttg cca cct gag gga gga aag cca tat ttg			2400
Lys Glu Lys Leu Ser Ala Leu Pro Pro Glu Gly Gly Lys Pro Tyr Leu			
785	790	795	800
gaa tct ttt aag ctc agt tta gat aac aca aaa gat acc ctg tta cct			2448
Glu Ser Phe Lys Leu Ser Leu Asp Asn Thr Lys Asp Thr Leu Leu Pro			
805	810	815	
gat gaa gtt tca aca ttg agc aaa aag gag aaa att cct ttg cag atg			2496
Asp Glu Val Ser Thr Leu Ser Lys Lys Glu Lys Ile Pro Leu Gln Met			
820	825	830	

gag gag ctc agt act gca gtt tat tca aat gat gac tta ttt att tct			2544
Glu Glu Leu Ser Thr Ala Val Tyr Ser Asn Asp Asp Leu Phe Ile Ser			
835	840	845	
aag gaa gca cag ata aga gaa act gaa acg ttt tca gat tca tct cca			2592
Lys Glu Ala Gln Ile Arg Glu Thr Glu Thr Phe Ser Asp Ser Ser Pro			
850	855	860	
att gaa att ata gat gag ttc cct aca ttg atc agt tct aaa act gat			2640
Ile Glu Ile Ile Asp Glu Phe Pro Thr Leu Ile Ser Ser Lys Thr Asp			
865	870	875	880
tca ttt tct aaa tta gcc agg gaa tat act gac cta gaa gta tcc cac			2688
Ser Phe Ser Lys Leu Ala Arg Glu Tyr Thr Asp Leu Glu Val Ser His			
885	890	895	
aaa agt gaa att gct aat gcc ccg gat gga gct ggg tca ttg cct tgc			2736
Lys Ser Glu Ile Ala Asn Ala Pro Asp Gly Ala Gly Ser Leu Pro Cys			
900	905	910	
aca gaa ttg ccc cat gac ctt tct ttg aag aac ata caa ccc aaa gtt			2784
Thr Glu Leu Pro His Asp Leu Ser Leu Lys Asn Ile Gln Pro Lys Val			
915	920	925	
gaa gag aaa atc agt ttc tca gat gac ttt tct aaa aat ggg tct gct			2832
Glu Glu Lys Ile Ser Phe Ser Asp Asp Phe Ser Lys Asn Gly Ser Ala			
930	935	940	
aca tca aag gtg ctc tta ttg cct cca gat gtt tct gct ttg gcc act			2880
Thr Ser Lys Val Leu Leu Pro Pro Asp Val Ser Ala Leu Ala Thr			
945	950	955	960
caa gca gag ata gag agc ata gtt aaa ccc aaa gtt ctt gtg aaa gaa			2928
Gln Ala Glu Ile Glu Ser Ile Val Lys Pro Lys Val Leu Val Lys Glu			
965	970	975	

gct gag aaa aaa ctt cct tcc gat aca gaa aaa gag gac aga tca cca	2976	
Ala Glu Lys Lys Leu Pro Ser Asp Thr Glu Lys Glu Asp Arg Ser Pro		
980	985	990
tct gct ata ttt tca gca gag ctg agt aaa act tca gtt gtt gac ctc	3024	
Ser Ala Ile Phe Ser Ala Glu Leu Ser Lys Thr Ser Val Val Asp Leu		
995	1000	1005
ctg tac tgg aga gac att aag aag act gga gtg gtg ttt ggt gcc	3069	
Leu Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val Val Phe Gly Ala		
1010	1015	1020
agc cta ttc ctg ctg ctt tca ttg aca gta ttc agc att gtg agc	3114	
Ser Leu Phe Leu Leu Leu Ser Leu Thr Val Phe Ser Ile Val Ser		
1025	1030	1035
gta aca gcc tac att gcc ttg gcc ctg ctc tct gtg acc atc agc	3159	
Val Thr Ala Tyr Ile Ala Leu Ala Leu Leu Ser Val Thr Ile Ser		
1040	1045	1050
ttt agg ata tac aag ggt gtg atc caa gct atc cag aaa tca gat	3204	
Phe Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile Gln Lys Ser Asp		
1055	1060	1065
gaa ggc cac cca ttc agg gca tat ctg gaa tct gaa gtt gct ata	3249	
Glu Gly His Pro Phe Arg Ala Tyr Leu Glu Ser Glu Val Ala Ile		
1070	1075	1080
tct gag gag ttg gtt cag aag tac agt aat tct gct ctt ggt cat	3294	
Ser Glu Glu Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly His		
1085	1090	1095
gtg aac tgc acg ata aag gaa ctc agg cgc ctc ttc tta gtt gat	3339	
Val Asn Cys Thr Ile Lys Glu Leu Arg Arg Leu Phe Leu Val Asp		
1100	1105	1110
gat tta gtt gat tct ctg aag ttt gca gtg ttg atg tgg gta ttt	3384	

Asp Leu Val Asp Ser Leu Lys Phe Ala Val Leu Met Trp Val Phe		
1115	1120	1125
acc tat gtt ggt gcc ttg ttt aat ggt ctg aca cta ctg att ttg		3429
Thr Tyr Val Gly Ala Leu Phe Asn Gly Leu Thr Leu Leu Ile Leu		
1130	1135	1140
gct ctc att tca ctc ttc agt gtt cct gtt att tat gaa cgg cat		3474
Ala Leu Ile Ser Leu Phe Ser Val Pro Val Ile Tyr Glu Arg His		
1145	1150	1155
cag gca cag ata gat cat tat cta gga ctt gca aat aag aat gtt		3519
Gln Ala Gln Ile Asp His Tyr Leu Gly Leu Ala Asn Lys Asn Val		
1160	1165	1170
aaa gat gct atg gct aaa atc caa gca aaa atc cct gga ttg aag		3564
Lys Asp Ala Met Ala Lys Ile Gln Ala Lys Ile Pro Gly Leu Lys		
1175	1180	1185
cgc aaa gct gaa tga aaacgccccaa aataattagt aggagttcat ctttaaaggg		3619
Arg Lys Ala Glu		
1190		
gatattcatt tgattatacg ggggagggtc aggaaagaac gaaccttgac gttgcagtgc		3679
agtttcacag atcggtgtta gatctttatt tttagccatg cactgttgtg aggaaaaatt		3739
acctgtcttg actgccatgt gttcatcatc ttaagtattt taagctgcta tgtatggatt		3799
taaacccgtaa tcatatcttt ttcctatctg aggcaactgggt ggaataaaaaa acctgtatat		3859
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<211> 1192

<212> PRT

<213> Homo sapiens

<400> 5

Met Glu Asp Leu Asp Gln Ser Pro Leu Val Ser Ser Ser Asp Ser Pro  
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20 25 30

Asp Glu Glu Glu Glu Glu Glu Glu Asp Glu Asp Glu Asp  
35 40 45

Leu Glu Glu Leu Glu Val Leu Glu Arg Lys Pro Ala Ala Gly Leu Ser  
50 55 60

Ala Ala Pro Val Pro Thr Ala Pro Ala Ala Gly Ala Pro Leu Met Asp  
65 70 75 80

Phe Gly Asn Asp Phe Val Pro Pro Ala Pro Arg Gly Pro Leu Pro Ala  
85 90 95

Ala Pro Pro Val Ala Pro Glu Arg Gln Pro Ser Trp Asp Pro Ser Pro  
100 105 110

Val Ser Ser Thr Val Pro Ala Pro Ser Pro Leu Ser Ala Ala Ala Val

115

120

125

Ser Pro Ser Lys Leu Pro Glu Asp Asp Glu Pro Pro Ala Arg Pro Pro

130

135

140

Pro Pro Pro Pro Ala Ser Val Ser Pro Gln Ala Glu Pro Val Trp Thr

145

150

155

160

Pro Pro Ala Pro Ala Pro Ala Ala Pro Pro Ser Thr Pro Ala Ala Pro

165

170

175

Lys Arg Arg Gly Ser Ser Gly Ser Val Asp Glu Thr Leu Phe Ala Leu

180

185

190

Pro Ala Ala Ser Glu Pro Val Ile Arg Ser Ser Ala Glu Asn Met Asp

195

200

205

Leu Lys Glu Gln Pro Gly Asn Thr Ile Ser Ala Gly Gln Glu Asp Phe

210

215

220

Pro Ser Val Leu Leu Glu Thr Ala Ala Ser Leu Pro Ser Leu Ser Pro

225

230

235

240

Leu Ser Ala Ala Ser Phe Lys Glu His Glu Tyr Leu Gly Asn Leu Ser

245

250

255

Thr Val Leu Pro Thr Glu Gly Thr Leu Gln Glu Asn Val Ser Glu Ala  
260 265 270

Ser Lys Glu Val Ser Glu Lys Ala Lys Thr Leu Leu Ile Asp Arg Asp  
275 280 285

Leu Thr Glu Phe Ser Glu Leu Glu Tyr Ser Glu Met Gly Ser Ser Phe  
290 295 300

Ser Val Ser Pro Lys Ala Glu Ser Ala Val Ile Val Ala Asn Pro Arg  
305 310 315 320

Glu Glu Ile Ile Val Lys Asn Lys Asp Glu Glu Glu Lys Leu Val Ser  
325 330 335

Asn Asn Ile Leu His Asn Gln Gln Glu Leu Pro Thr Ala Leu Thr Lys  
340 345 350

Leu Val Lys Glu Asp Glu Val Val Ser Ser Glu Lys Ala Lys Asp Ser  
355 360 365

Phe Asn Glu Lys Arg Val Ala Val Glu Ala Pro Met Arg Glu Glu Tyr  
370 375 380

Ala Asp Phe Lys Pro Phe Glu Arg Val Trp Glu Val Lys Asp Ser Lys  
385 390 395 400

Glu Asp Ser Asp Met Leu Ala Ala Gly Gly Lys Ile Glu Ser Asn Leu

405

410

415

Glu Ser Lys Val Asp Lys Lys Cys Phe Ala Asp Ser Leu Glu Gln Thr

420

425

430

Asn His Glu Lys Asp Ser Glu Ser Ser Asn Asp Asp Thr Ser Phe Pro

435

440

445

Ser Thr Pro Glu Gly Ile Lys Asp Arg Ser Gly Ala Tyr Ile Thr Cys

450

455

460

Ala Pro Phe Asn Pro Ala Ala Thr Glu Ser Ile Ala Thr Asn Ile Phe

465

470

475

480

Pro Leu Leu Gly Asp Pro Thr Ser Glu Asn Lys Thr Asp Glu Lys Lys

485

490

495

Ile Glu Glu Lys Lys Ala Gln Ile Val Thr Glu Lys Asn Thr Ser Thr

500

505

510

Lys Thr Ser Asn Pro Phe Leu Val Ala Ala Gln Asp Ser Glu Thr Asp

515

520

525

Tyr Val Thr Thr Asp Asn Leu Thr Lys Val Thr Glu Glu Val Val Ala

530

535

540

Asn Met Pro Glu Gly Leu Thr Pro Asp Leu Val Gln Glu Ala Cys Glu

545

550

555

560

Ser Glu Leu Asn Glu Val Thr Gly Thr Lys Ile Ala Tyr Glu Thr Lys  
565 570 575

Met Asp Leu Val Gln Thr Ser Glu Val Met Gln Glu Ser Leu Tyr Pro  
580 585 590

Ala Ala Gln Leu Cys Pro Ser Phe Glu Glu Ser Glu Ala Thr Pro Ser  
595 600 605

Pro Val Leu Pro Asp Ile Val Met Glu Ala Pro Leu Asn Ser Ala Val  
610 615 620

Pro Ser Ala Gly Ala Ser Val Ile Gln Pro Ser Ser Ser Pro Leu Glu  
625 630 635 640

Ala Ser Ser Val Asn Tyr Glu Ser Ile Lys His Glu Pro Glu Asn Pro  
645 650 655

Pro Pro Tyr Glu Glu Ala Met Ser Val Ser Leu Lys Lys Val Ser Gly  
660 665 670

Ile Lys Glu Glu Ile Lys Glu Pro Glu Asn Ile Asn Ala Ala Leu Gln  
675 680 685

Glu Thr Glu Ala Pro Tyr Ile Ser Ile Ala Cys Asp Leu Ile Lys Glu  
690 695 700

Thr Lys Leu Ser Ala Glu Pro Ala Pro Asp Phe Ser Asp Tyr Ser Glu  
705 710 715 720

Met Ala Lys Val Glu Gln Pro Val Pro Asp His Ser Glu Leu Val Glu  
725 730 735

Asp Ser Ser Pro Asp Ser Glu Pro Val Asp Leu Phe Ser Asp Asp Ser  
740 745 750

Ile Pro Asp Val Pro Gln Lys Gln Asp Glu Thr Val Met Leu Val Lys  
755 760 765

Glu Ser Leu Thr Glu Thr Ser Phe Glu Ser Met Ile Glu Tyr Glu Asn  
770 775 780

Lys Glu Lys Leu Ser Ala Leu Pro Pro Glu Gly Gly Lys Pro Tyr Leu  
785 790 795 800

Glu Ser Phe Lys Leu Ser Leu Asp Asn Thr Lys Asp Thr Leu Leu Pro  
805 810 815

Asp Glu Val Ser Thr Leu Ser Lys Lys Glu Lys Ile Pro Leu Gln Met  
820 825 830

Glu Glu Leu Ser Thr Ala Val Tyr Ser Asn Asp Asp Leu Phe Ile Ser  
835 840 845

Lys Glu Ala Gln Ile Arg Glu Thr Glu Thr Phe Ser Asp Ser Ser Pro  
850 855 860

Ile Glu Ile Ile Asp Glu Phe Pro Thr Leu Ile Ser Ser Lys Thr Asp  
865 870 875 880

Ser Phe Ser Lys Leu Ala Arg Glu Tyr Thr Asp Leu Glu Val Ser His  
885 890 895

Lys Ser Glu Ile Ala Asn Ala Pro Asp Gly Ala Gly Ser Leu Pro Cys  
900 905 910

Thr Glu Leu Pro His Asp Leu Ser Leu Lys Asn Ile Gln Pro Lys Val  
915 920 925

Glu Glu Lys Ile Ser Phe Ser Asp Asp Phe Ser Lys Asn Gly Ser Ala  
930 935 940

Thr Ser Lys Val Leu Leu Leu Pro Pro Asp Val Ser Ala Leu Ala Thr  
945 950 955 960

Gln Ala Glu Ile Glu Ser Ile Val Lys Pro Lys Val Leu Val Lys Glu  
965 970 975

Ala Glu Lys Lys Leu Pro Ser Asp Thr Glu Lys Glu Asp Arg Ser Pro  
980 985 990

Ser Ala Ile Phe Ser Ala Glu Leu Ser Lys Thr Ser Val Val Asp Leu

995

1000

1005

Leu Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val Val Phe Gly Ala  
1010 1015 1020

Ser Leu Phe Leu Leu Leu Ser Leu Thr Val Phe Ser Ile Val Ser  
1025 1030 1035

Val Thr Ala Tyr Ile Ala Leu Ala Leu Leu Ser Val Thr Ile Ser  
1040 1045 1050

Phe Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile Gln Lys Ser Asp  
1055 1060 1065

Glu Gly His Pro Phe Arg Ala Tyr Leu Glu Ser Glu Val Ala Ile  
1070 1075 1080

Ser Glu Glu Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly His  
1085 1090 1095

Val Asn Cys Thr Ile Lys Glu Leu Arg Arg Leu Phe Leu Val Asp  
1100 1105 1110

Asp Leu Val Asp Ser Leu Lys Phe Ala Val Leu Met Trp Val Phe  
1115 1120 1125

Thr Tyr Val Gly Ala Leu Phe Asn Gly Leu Thr Leu Leu Ile Leu  
1130 1135 1140

Ala Leu Ile Ser Leu Phe Ser Val Pro Val Ile Tyr Glu Arg His  
1145 1150 1155

Gln Ala Gln Ile Asp His Tyr Leu Gly Leu Ala Asn Lys Asn Val  
1160 1165 1170

Lys Asp Ala Met Ala Lys Ile Gln Ala Lys Ile Pro Gly Leu Lys  
1175 1180 1185

Arg Lys Ala Glu  
1190

<210> 6

<211> 18

<212> PRT

<213> Homo sapiens

<220>

<221> PEPTIDE

<222> (1)..(18)

<223> Human NogoA\_623-640

<400> 6

Asn Tyr Glu Ser Ile Lys His Glu Pro Glu Asn Pro Pro Pro Tyr Glu  
1 5 10 15

Glu Ala

<210> 7

<211> 819

<212> PRT

<213> Homo sapiens

<220>

<221> PEPTIDE

<222> (1)..(819)

<223> human Nig

<400> 7

Asp Glu Thr Leu Phe Ala Leu Pro Ala Ala Ser Glu Pro Val Ile Arg  
1 5 10 15

Ser Ser Ala Glu Asn Met Asp Leu Lys Glu Gln Pro Gly Asn Thr Ile

20

25

30

Ser Ala Gly Gln Glu Asp Phe Pro Ser Val Leu Leu Glu Thr Ala Ala

35

40

45

Ser Leu Pro Ser Leu Ser Pro Leu Ser Ala Ala Ser Phe Lys Glu His

50

55

60

Glu Tyr Leu Gly Asn Leu Ser Thr Val Leu Pro Thr Glu Gly Thr Leu

65

70

75

80

Gln Glu Asn Val Ser Glu Ala Ser Lys Glu Val Ser Glu Lys Ala Lys

85

90

95

Thr Leu Leu Ile Asp Arg Asp Leu Thr Glu Phe Ser Glu Leu Glu Tyr

100

105

110

Ser Glu Met Gly Ser Ser Phe Ser Val Ser Pro Lys Ala Glu Ser Ala

115

120

125

Val Ile Val Ala Asn Pro Arg Glu Glu Ile Ile Val Lys Asn Lys Asp

130

135

140

Glu Glu Glu Lys Leu Val Ser Asn Asn Ile Leu His Asn Gln Gln Glu

145

150

155

160

Leu Pro Thr Ala Leu Thr Lys Leu Val Lys Glu Asp Glu Val Val Ser  
165 170 175

Ser Glu Lys Ala Lys Asp Ser Phe Asn Glu Lys Arg Val Ala Val Glu  
180 185 190

Ala Pro Met Arg Glu Glu Tyr Ala Asp Phe Lys Pro Phe Glu Arg Val  
195 200 205

Trp Glu Val Lys Asp Ser Lys Glu Asp Ser Asp Met Leu Ala Ala Gly  
210 215 220

Gly Lys Ile Glu Ser Asn Leu Glu Ser Lys Val Asp Lys Lys Cys Phe  
225 230 235 240

Ala Asp Ser Leu Glu Gln Thr Asn His Glu Lys Asp Ser Glu Ser Ser  
245 250 255

Asn Asp Asp Thr Ser Phe Pro Ser Thr Pro Glu Gly Ile Lys Asp Arg  
260 265 270

Ser Gly Ala Tyr Ile Thr Cys Ala Pro Phe Asn Pro Ala Ala Thr Glu  
275 280 285

Ser Ile Ala Thr Asn Ile Phe Pro Leu Leu Gly Asp Pro Thr Ser Glu  
290 295 300

Asn Lys Thr Asp Glu Lys Lys Ile Glu Glu Lys Ala Gln Ile Val

305

310

315

320

Thr Glu Lys Asn Thr Ser Thr Lys Thr Ser Asn Pro Phe Leu Val Ala  
325 330 335

Ala Gln Asp Ser Glu Thr Asp Tyr Val Thr Thr Asp Asn Leu Thr Lys  
340 345 350

Val Thr Glu Glu Val Val Ala Asn Met Pro Glu Gly Leu Thr Pro Asp  
355 360 365

Leu Val Gln Glu Ala Cys Glu Ser Glu Leu Asn Glu Val Thr Gly Thr  
370 375 380

Lys Ile Ala Tyr Glu Thr Lys Met Asp Leu Val Gln Thr Ser Glu Val  
385 390 395 400

Met Gln Glu Ser Leu Tyr Pro Ala Ala Gln Leu Cys Pro Ser Phe Glu  
405 410 415

Glu Ser Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val Met Glu  
420 425 430

Ala Pro Leu Asn Ser Ala Val Pro Ser Ala Gly Ala Ser Val Ile Gln  
435 440 445

Pro Ser Ser Ser Pro Leu Glu Ala Ser Ser Val Asn Tyr Glu Ser Ile  
450 455 460

Lys His Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu Ala Met Ser Val  
465 470 475 480

Ser Leu Lys Lys Val Ser Gly Ile Lys Glu Glu Ile Lys Glu Pro Glu  
485 490 495

Asn Ile Asn Ala Ala Leu Gln Glu Thr Glu Ala Pro Tyr Ile Ser Ile  
500 505 510

Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser Ala Glu Pro Ala Pro  
515 520 525

Asp Phe Ser Asp Tyr Ser Glu Met Ala Lys Val Glu Gln Pro Val Pro  
530 535 540

Asp His Ser Glu Leu Val Glu Asp Ser Ser Pro Asp Ser Glu Pro Val  
545 550 555 560

Asp Leu Phe Ser Asp Asp Ser Ile Pro Asp Val Pro Gln Lys Gln Asp  
565 570 575

Glu Thr Val Met Leu Val Lys Glu Ser Leu Thr Glu Thr Ser Phe Glu  
580 585 590

Ser Met Ile Glu Tyr Glu Asn Lys Glu Lys Leu Ser Ala Leu Pro Pro  
595 600 605

Glu Gly Gly Lys Pro Tyr Leu Glu Ser Phe Lys Leu Ser Leu Asp Asn

610 615 620

Thr Lys Asp Thr Leu Leu Pro Asp Glu Val Ser Thr Leu Ser Lys Lys

625 630 635 640

Glu Lys Ile Pro Leu Gln Met Glu Glu Leu Ser Thr Ala Val Tyr Ser

645 650 655

Asn Asp Asp Leu Phe Ile Ser Lys Glu Ala Gln Ile Arg Glu Thr Glu

660 665 670

Thr Phe Ser Asp Ser Ser Pro Ile Glu Ile Ile Asp Glu Phe Pro Thr

675 680 685

Leu Ile Ser Ser Lys Thr Asp Ser Phe Ser Lys Leu Ala Arg Glu Tyr

690 695 700

Thr Asp Leu Glu Val Ser His Lys Ser Glu Ile Ala Asn Ala Pro Asp

705 710 715 720

Gly Ala Gly Ser Leu Pro Cys Thr Glu Leu Pro His Asp Leu Ser Leu

725 730 735

Lys Asn Ile Gln Pro Lys Val Glu Glu Lys Ile Ser Phe Ser Asp Asp

740 745 750

Phe Ser Lys Asn Gly Ser Ala Thr Ser Lys Val Leu Leu Leu Pro Pro  
755 760 765

Asp Val Ser Ala Leu Ala Thr Gln Ala Glu Ile Glu Ser Ile Val Lys  
770 775 780

Pro Lys Val Leu Val Lys Glu Ala Glu Lys Lys Leu Pro Ser Asp Thr  
785 790 795 800

Glu Lys Glu Asp Arg Ser Pro Ser Ala Ile Phe Ser Ala Glu Leu Ser  
805 810 815

Lys Thr Ser

<210> 8

<211> 10

<212> PRT

<213> *Mus musculus*

<220>

<221> BINDING

<222> (1)..(10)

<223> hypervariable part of heavy chain of 11C7

<400> 8

Gly Phe Asp Phe Arg Arg Asn Trp Met Ser  
1 5 10

<210> 9

<211> 17

<212> PRT

<213> *Mus musculus*

<220>

<221> BINDING

<222> (1) .. (17)

<223> hypervariable part of heavy chain of 11C7

<400> 9

Glu Ile Asn Pro Asp Ser Ser Lys Ile Asn Tyr Thr Pro Ser Leu Lys  
1 5 10 15

Asp

<210> 10

<211> 9

<212> PRT

<213> *Mus musculus*

<220>

<221> BINDING

<222> (1)..(9)

<223> hypervariable part of heavy chain of 11C7

<400> 10

Pro Val Trp Met Tyr Ala Met Asp Tyr

1

5

<210> 11

<211> 16

<212> PRT

<213> *Mus musculus*

<220>

<221> BINDING

<222> (1)..(16)

<223> hypervariable part of light chain of 11C7

<400> 11

Lys Ser Ser Gln Ser Leu Leu His Ser Asp Gly Lys Thr Tyr Leu Asn  
1 5 10 15

<210> 12

<211> 7

<212> PRT

<213> *Mus musculus*

<220>

<221> BINDING

<222> (1)..(7)

<223> hypervariable part of light chain of 11C7

<400> 12

Leu Val Ser Lys Leu Asp Ser  
1 5

<210> 13

<211> 9

<212> PRT

<213> *Mus musculus*

<220>

<221> BINDING

<222> (1) .. (9)

<223> hypervariable part of light chain of 11C7

<400> 13

Trp Gln Gly Thr His Phe Pro Gln Thr  
1 5

<210> 14

<211> 30

<212> DNA

<213> *Mus musculus*

<220>

<221> misc\_binding

<222> (1) .. (30)

<223> DNA-CDR1-11C7

<400> 14

ggattcgatt ttagaagaaa ttggatgagt

30

<210> 15

<211> 51

<212> DNA

<213> *Mus musculus*

<220>

<221> misc\_binding

<222> (1)..(51)

<223> DNA-CDR2-11C7

<400> 15

gaaattaatc cagatagcag taagataaaac tatacgccat ctctaaagga t 51

<210> 16

<211> 27

<212> DNA

<213> *Mus musculus*

<220>

<221> misc\_binding

<222> (1)..(27)

<223> DNA-CDR3-11C7

<400> 16

ccgggtctggaa tgtatgctat ggactac 27

<210> 17

<211> 48

<212> DNA

<213> Mus musculus

<220>

<221> misc\_binding

<222> (1)..(48)

<223> DNA-CDR'1-11C7

<400> 17

aagtcaagtc agagcctctt gcatagtgat ggaaagacat atttgaat

48

<210> 18

<211> 21

<212> DNA

<213> Mus musculus

<220>

<221> misc\_binding

<222> (1) .. (21)

<223> DNA-CDR'2-11C7

<400> 18

ctgggtgtctta aactggactc t

21

<210> 19

<211> 27

<212> DNA

<213> *Mus musculus*

<220>

<221> misc\_binding

<222> (1) .. (27)

<223> DNA-CDR'3-11C7

<400> 19

tggcaaggta cacatttcc tcagacg

27

<210> 20

<211> 54

<212> DNA

<213> *Mus musculus*

<220>

<221> CDS

<222> (1)..(54)

<223> leader sequence for heavy chain of 11C7

<400> 20

atg gat ttt ggg ctg att ttt ttt att gtt ggt ctt tta aaa ggg gtc  
Met Asp Phe Gly Leu Ile Phe Phe Ile Val Gly Leu Leu Lys Gly Val  
1 5 10 15

48

cag tgt  
Gln Cys

54

<210> 21

<211> 18

<212> PRT

<213> *Mus musculus*

<400> 21

Met Asp Phe Gly Leu Ile Phe Phe Ile Val Gly Leu Leu Lys Gly Val  
1 5 10 15

Gln Cys

<210> 22

<211> 57

<212> DNA

<213> *Mus musculus*

<220>

<221> CDS

<222> (1) .. (57)

<223> leader sequence for 11C7-light chain

<400> 22

atg agt cct gcc cag ttc ctg ttt ctg tta gtg ctc tgg att cgg gaa 48  
Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu Trp Ile Arg Glu  
1 5 10 15

acc agc ggt  
Thr Ser Gly

57

<210> 23

<211> 19

<212> PRT

<213> Mus musculus

<400> 23

Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu Trp Ile Arg Glu  
1 5 10 15

Thr Ser Gly

<210> 24

<211> 181

<212> PRT

<213> Homo sapiens

<220>

<221> PEPTIDE

<222> (1)..(181)

<223> human Nig-D20

<400> 24

Gly Thr Lys Ile Ala Tyr Glu Thr Lys Met Asp Leu Val Gln Thr Ser  
1 5 10 15

Glu Val Met Gln Glu Ser Leu Tyr Pro Ala Ala Gln Leu Cys Pro Ser  
20 25 30

Phe Glu Glu Ser Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val  
35 40 45

Met Glu Ala Pro Leu Asn Ser Ala Val Pro Ser Ala Gly Ala Ser Val  
50 55 60

Ile Gln Pro Ser Ser Ser Pro Leu Glu Ala Ser Ser Val Asn Tyr Glu  
65 70 75 80

Ser Ile Lys His Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu Ala Met  
85 90 95

Ser Val Ser Leu Lys Lys Val Ser Gly Ile Lys Glu Glu Ile Lys Glu  
100 105 110

Pro Glu Asn Ile Asn Ala Ala Leu Gln Glu Thr Glu Ala Pro Tyr Ile

115

120

125

Ser Ile Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser Ala Glu Pro

130

135

140

Ala Pro Asp Phe Ser Asp Tyr Ser Glu Met Ala Lys Val Glu Gln Pro

145

150

155

160

Val Pro Asp His Ser Glu Leu Val Glu Asp Ser Ser Pro Asp Ser Glu

165

170

175

Pro Val Asp Leu Phe

180

<210> 25

<211> 3492

<212> DNA

<213> Rattus norvegicus

<220>

<221> CDS

<222> (1)..(3492)

&lt;223&gt; rat NogoA

&lt;400&gt; 25

atg gaa gac ata gac cag tcg tcg ctg gtc tcc tcg tcc acg gac agc 48

Met Glu Asp Ile Asp Gln Ser Ser Leu Val Ser Ser Ser Thr Asp Ser

1 5 10 15

ccg ccc cgg cct ccg ccc gcc ttc aag tac cag ttc gtg acg gag ccc 96

Pro Pro Arg Pro Pro Ala Phe Lys Tyr Gln Phe Val Thr Glu Pro

20 25 30

gag gac gag gag gac gag gag gag gag gag gag gag gag gac gac 144

Glu Asp Glu Asp Glu Glu Glu Glu Asp Glu Glu Asp Asp Asp

35 40 45

gag gac cta gag gaa ctg gag gtg ctg gag agg aag ccc gca gcc ggg 192

Glu Asp Leu Glu Glu Leu Glu Val Leu Glu Arg Lys Pro Ala Ala Gly

50 55 60

ctg tcc gca gct gcg gtg ccg ccc gcc gcc gcc gcg ccg ctg ctg gac 240

Leu Ser Ala Ala Ala Val Pro Pro Ala Ala Ala Pro Leu Leu Asp

65 70 75 80

ttc agc agc gac tcg gtg ccc ccc gcg ccc cgc ggg ccg ctg ccg gcc 288

Phe Ser Ser Asp Ser Val Pro Pro Ala Pro Arg Gly Pro Leu Pro Ala

85 90 95

gcg ccc cct gcc gct cct gag agg cag cca tcc tgg gaa cgc agc ccc 336

Ala Pro Pro Ala Ala Pro Glu Arg Gln Pro Ser Trp Glu Arg Ser Pro

100 105 110

gcg gcg ccc gcg cca tcc ctg ccg ccc gct gcc gca gtc ctg ccc tcc 384

Ala Ala Pro Ala Pro Ser Leu Pro Pro Ala Ala Val Leu Pro Ser

115 120 125

aag ctc cca gag gac gac gag cct ccg gcg agg ccc ccg cct ccg ccg	432
Lys Leu Pro Glu Asp Asp Glu Pro Pro Ala Arg Pro Pro Pro Pro	
130 135 140	
cca gcc ggc gcg agc ccc ctg gcg gag ccc gcc gcg ccc cct tcc acg	480
Pro Ala Gly Ala Ser Pro Leu Ala Glu Pro Ala Ala Pro Pro Ser Thr	
145 150 155 160	
ccg gcc gcg ccc aag cgc agg ggc tcc ggc tca gtg gat gag acc ctt	528
Pro Ala Ala Pro Lys Arg Arg Gly Ser Gly Ser Val Asp Glu Thr Leu	
165 170 175	
ttt gct ctt cct gct gca tct gag cct gtg ata ccc tcc tct gca gaa	576
Phe Ala Leu Pro Ala Ala Ser Glu Pro Val Ile Pro Ser Ser Ala Glu	
180 185 190	
aaa att atg gat ttg atg gag cag cca ggt aac act gtt tcg tct ggt	624
Lys Ile Met Asp Leu Met Glu Gln Pro Gly Asn Thr Val Ser Ser Gly	
195 200 205	
caa gag gat ttc cca tct gtc ctg ctt gaa act gct gcc tct ctt cct	672
Gln Glu Asp Phe Pro Ser Val Leu Leu Glu Thr Ala Ala Ser Leu Pro	
210 215 220	
tct cta tct cct ctc tca act gtt tct ttt aaa gaa cat gga tac ctt	720
Ser Leu Ser Pro Leu Ser Thr Val Ser Phe Lys Glu His Gly Tyr Leu	
225 230 235 240	
ggt aac tta tca gca gtg tca tcc tca gaa gga aca att gaa gaa act	768
Gly Asn Leu Ser Ala Val Ser Ser Glu Gly Thr Ile Glu Glu Thr	
245 250 255	
tta aat gaa gct tct aaa gag ttg cca gag agg gca aca aat cca ttt	816
Leu Asn Glu Ala Ser Lys Glu Leu Pro Glu Arg Ala Thr Asn Pro Phe	
260 265 270	
gta aat aga gat tta gca gaa ttt tca gaa tta gaa tat tca gaa atg	864

Val Asn Arg Asp Leu Ala Glu Phe Ser Glu Leu Glu Tyr Ser Glu Met  
275 280 285

gga tca tct ttt aaa ggc tcc cca aaa gga gag tca gcc ata tta gta 912  
Gly Ser Ser Phe Lys Gly Ser Pro Lys Gly Glu Ser Ala Ile Leu Val  
290 295 300

gaa aac act aag gaa gaa gta att gtg agg agt aaa gac aaa gag gat 960  
Glu Asn Thr Lys Glu Glu Val Ile Val Arg Ser Lys Asp Lys Glu Asp  
305 310 315 320

tta gtt tgt agt gca gcc ctt cac agt cca caa gaa tca cct gtg ggt 1008  
Leu Val Cys Ser Ala Ala Leu His Ser Pro Gln Glu Ser Pro Val Gly  
325 330 335

aaa gaa gac aga gtt gtg tct cca gaa aag aca atg gac att ttt aat 1056  
Lys Glu Asp Arg Val Val Ser Pro Glu Lys Thr Met Asp Ile Phe Asn  
340 345 350

gaa atg cag atg tca gta gta gca cct gtg agg gaa gag tat gca gac 1104  
Glu Met Gln Met Ser Val Val Ala Pro Val Arg Glu Glu Tyr Ala Asp  
355 360 365

ttt aag cca ttt gaa caa gca tgg gaa gtg aaa gat act tat gag gga 1152  
Phe Lys Pro Phe Glu Gln Ala Trp Glu Val Lys Asp Thr Tyr Glu Gly  
370 375 380

agt agg gat gtg ctg gct gct aga gct aat gtg gaa agt aaa gtg gac 1200  
Ser Arg Asp Val Leu Ala Ala Arg Ala Asn Val Glu Ser Lys Val Asp  
385 390 395 400

aga aaa tgc ttg gaa gat agc ctg gag caa aaa agt ctt ggg aag gat 1248  
Arg Lys Cys Leu Glu Asp Ser Leu Glu Gln Lys Ser Leu Gly Lys Asp  
405 410 415

agt gaa ggc aga aat gag gat gct tct ttc ccc agt acc cca gaa cct 1296  
Ser Glu Gly Arg Asn Glu Asp Ala Ser Phe Pro Ser Thr Pro Glu Pro

420	425	430	
gtg aag gac agc tcc aga gca tat att acc tcc tgt gct tcc ttt acc tca Val Lys Asp Ser Ser Arg Ala Tyr Ile Thr Cys Ala Ser Phe Thr Ser			1344
435	440	445	
gca acc gaa agc acc aca gca aac act ttc cct ttg tta gaa gat cat Ala Thr Glu Ser Thr Ala Asn Thr Phe Pro Leu Leu Glu Asp His			1392
450	455	460	
act tca gaa aat aaa aca gat gaa aaa aaa ata gaa gaa agg aag gcc Thr Ser Glu Asn Lys Thr Asp Glu Lys Lys Ile Glu Glu Arg Lys Ala			1440
465	470	475	480
caa att ata aca gag aag act agc ccc aaa acg tca aat cct ttc ctt Gln Ile Ile Thr Glu Lys Thr Ser Pro Lys Thr Ser Asn Pro Phe Leu			1488
485	490	495	
gta gca gta cag gat tct gag gca gat tat gtt aca aca gat acc tta Val Ala Val Gln Asp Ser Glu Ala Asp Tyr Val Thr Thr Asp Thr Leu			1536
500	505	510	
tca aag gtg act gag gca gca gtg tca aac atg cct gaa ggt ctg acg Ser Lys Val Thr Glu Ala Ala Val Ser Asn Met Pro Glu Gly Leu Thr			1584
515	520	525	
cca gat tta gtt cag gaa gca tgt gaa agt gaa ctg aat gaa gcc aca Pro Asp Leu Val Gln Glu Ala Cys Glu Ser Glu Leu Asn Glu Ala Thr			1632
530	535	540	
ggt aca aag att gct tat gaa aca aaa gtg gac ttg gtc caa aca tca Gly Thr Lys Ile Ala Tyr Glu Thr Lys Val Asp Leu Val Gln Thr Ser			1680
545	550	555	560
gaa gct ata caa gaa tca ctt tac ccc aca gca cag ctt tgc cca tca Glu Ala Ile Gln Glu Ser Leu Tyr Pro Thr Ala Gln Leu Cys Pro Ser			1728
565	570	575	

ttt gag gaa gct gaa gca act ccg tca cca gtt ttg cct gat att gtt			1776
Phe Glu Glu Ala Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val			
580	585	590	
atg gaa gca cca tta aat tct ctc ctt cca agc gct ggt gct tct gta			1824
Met Glu Ala Pro Leu Asn Ser Leu Leu Pro Ser Ala Gly Ala Ser Val			
595	600	605	
gtg cag ccc agt gta tcc cca ctg gaa gca cct cct cca gtt agt tat			1872
Val Gln Pro Ser Val Ser Pro Leu Glu Ala Pro Pro Val Ser Tyr			
610	615	620	
gac agt ata aag ctt gag cct gaa aac ccc cca cca tat gaa gaa gcc			1920
Asp Ser Ile Lys Leu Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu Ala			
625	630	635	640
atg aat gta gca cta aaa gct ttg gga aca aag gaa gga ata aaa gag			1968
Met Asn Val Ala Leu Lys Ala Leu Gly Thr Lys Glu Gly Ile Lys Glu			
645	650	655	
cct gaa agt ttt aat gca gct gtt cag gaa aca gaa gct cct tat ata			2016
Pro Glu Ser Phe Asn Ala Ala Val Gln Glu Thr Glu Ala Pro Tyr Ile			
660	665	670	
tcc att gcg tgt gat tta att aaa gaa aca aag ctc tcc act gag cca			2064
Ser Ile Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser Thr Glu Pro			
675	680	685	
agt cca gat ttc tct aat tat tca gaa ata gca aaa ttc gag aag tcg			2112
Ser Pro Asp Phe Ser Asn Tyr Ser Glu Ile Ala Lys Phe Glu Lys Ser			
690	695	700	
gtg ccc gaa cac gct gag cta gtg gag gat tcc tca cct gaa tct gaa			2160
Val Pro Glu His Ala Glu Leu Val Glu Asp Ser Ser Pro Glu Ser Glu			
705	710	715	720

cca gtt gac tta ttt agt gat gat tcg att cct gaa gtc cca caa aca	2208		
Pro Val Asp Leu Phe Ser Asp Asp Ser Ile Pro Glu Val Pro Gln Thr			
725	730	735	
caa gag gag gct gtg atg ctc atg aag gag agt ctc act gaa gtg tct	2256		
Gln Glu Glu Ala Val Met Leu Met Lys Glu Ser Leu Thr Glu Val Ser			
740	745	750	
gag aca gta gcc cag cac aaa gag gag aga ctt agt gcc tca cct cag	2304		
Glu Thr Val Ala Gln His Lys Glu Glu Arg Leu Ser Ala Ser Pro Gln			
755	760	765	
gag cta gga aag cca tat tta gag tct ttt cag ccc aat tta cat agt	2352		
Glu Leu Gly Lys Pro Tyr Leu Glu Ser Phe Gln Pro Asn Leu His Ser			
770	775	780	
aca aaa gat gct gca tct aat gac att cca aca ttg acc aaa aag gag	2400		
Thr Lys Asp Ala Ala Ser Asn Asp Ile Pro Thr Leu Thr Lys Lys Glu			
785	790	795	800
aaa att tct ttg caa atg gaa gag ttt aat act gca att tat tca aat	2448		
Lys Ile Ser Leu Gln Met Glu Glu Phe Asn Thr Ala Ile Tyr Ser Asn			
805	810	815	
gat gac tta ctt tct tct aag gaa gac aaa ata aaa gaa agt gaa aca	2496		
Asp Asp Leu Leu Ser Ser Lys Glu Asp Lys Ile Lys Glu Ser Glu Thr			
820	825	830	
ttt tca gat tca tct ccg att gag ata ata gat gaa ttt ccc acg ttt	2544		
Phe Ser Asp Ser Ser Pro Ile Glu Ile Ile Asp Glu Phe Pro Thr Phe			
835	840	845	
gtc agt gct aaa gat gat tct cct aaa tta gcc aag gag tac act gat	2592		
Val Ser Ala Lys Asp Asp Ser Pro Lys Leu Ala Lys Glu Tyr Thr Asp			
850	855	860	
cta gaa gta tcc gac aaa agt gaa att gct aat atc caa agc ggg gca	2640		

Leu Glu Val Ser Asp Lys Ser Glu Ile Ala Asn Ile Gln Ser Gly Ala  
865 870 875 880

gat tca ttg cct tgc tta gaa ttg ccc tgt gac ctt tct ttc aag aat 2688  
Asp Ser Leu Pro Cys Leu Glu Leu Pro Cys Asp Leu Ser Phe Lys Asn  
885 890 895

ata tat cct aaa gat gaa gta cat gtt tca gat gaa ttc tcc gaa aat 2736  
Ile Tyr Pro Lys Asp Glu Val His Val Ser Asp Glu Phe Ser Glu Asn  
900 905 910

agg tcc agt gta tct aag gca tcc ata tcg cct tca aat gtc tct gct 2784  
Arg Ser Ser Val Ser Lys Ala Ser Ile Ser Pro Ser Asn Val Ser Ala  
915 920 925

ttg gaa cct cag aca gaa atg ggc agc ata gtt aaa tcc aaa tca ctt 2832  
Leu Glu Pro Gln Thr Glu Met Gly Ser Ile Val Lys Ser Lys Ser Leu  
930 935 940

acg aaa gaa gca gag aaa aaa ctt cct tct gac aca gag aaa gag gac 2880  
Thr Lys Glu Ala Glu Lys Lys Leu Pro Ser Asp Thr Glu Lys Glu Asp  
945 950 955 960

aga tcc ctg tca gct gta ttg tca gca gag ctg agt aaa act tca gtt 2928  
Arg Ser Leu Ser Ala Val Leu Ser Ala Glu Leu Ser Lys Thr Ser Val  
965 970 975

gtt gac ctc ctc tac tgg aga gac att aag aag act gga gtg gtg ttt 2976  
Val Asp Leu Leu Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val Val Phe  
980 985 990

ggt gcc agc tta ttc ctg ctg ctg tct ctg aca gtg ttc agc att gtc 3024  
Gly Ala Ser Leu Phe Leu Leu Leu Ser Leu Thr Val Phe Ser Ile Val  
995 1000 1005

agt gta acg gcc tac att gcc ttg gcc ctg ctc tcg gtg act atc 3069  
Ser Val Thr Ala Tyr Ile Ala Leu Ala Leu Leu Ser Val Thr Ile

1010	1015	1020	
agc ttt agg ata tat aag ggc gtg atc cag gct atc cag aaa tca			3114
Ser Phe Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile Gln Lys Ser			
1025	1030	1035	
gat gaa ggc cac cca ttc agg gca tat tta gaa tct gaa gtt gct			3159
Asp Glu Gly His Pro Phe Arg Ala Tyr Leu Glu Ser Glu Val Ala			
1040	1045	1050	
ata tca gag gaa ttg gtt cag aaa tac agt aat tct gct ctt ggt			3204
Ile Ser Glu Glu Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly			
1055	1060	1065	
cat gtg aac agc aca ata aaa gaa ctg agg cggtt ttc tta gtt			3249
His Val Asn Ser Thr Ile Lys Glu Leu Arg Arg Leu Phe Leu Val			
1070	1075	1080	
gat gat tta gtt gat tcc ctg aag ttt gca gtg ttg atg tgg gtg			3294
Asp Asp Leu Val Asp Ser Leu Lys Phe Ala Val Leu Met Trp Val			
1085	1090	1095	
ttt act tat gtt ggt gcc ttg ttc aat ggt ctg aca cta ctg att			3339
Phe Thr Tyr Val Gly Ala Leu Phe Asn Gly Leu Thr Leu Leu Ile			
1100	1105	1110	
tta gct ctg atc tca ctc ttc agt att cct gtt att tat gaa cggtt			3384
Leu Ala Leu Ile Ser Leu Phe Ser Ile Pro Val Ile Tyr Glu Arg			
1115	1120	1125	
cat cag gtg cag ata gat cat tat cta gga ctt gca aac aag agt			3429
His Gln Val Gln Ile Asp His Tyr Leu Gly Leu Ala Asn Lys Ser			
1130	1135	1140	
gtt aag gat gcc atg gcc aaa atc caa gca aaa atc cct gga ttg			3474
Val Lys Asp Ala Met Ala Lys Ile Gln Ala Lys Ile Pro Gly Leu			
1145	1150	1155	

aag cgc aaa gca gat tga 3492  
Lys Arg Lys Ala Asp  
1160

<210> 26

<211> 1163

<212> PRT

<213> Rattus norvegicus

<400> 26

Met Glu Asp Ile Asp Gln Ser Ser Leu Val Ser Ser Ser Thr Asp Ser  
1 5 10 15

Pro Pro Arg Pro Pro Pro Ala Phe Lys Tyr Gln Phe Val Thr Glu Pro  
20 25 30

Glu Asp Glu Glu Asp Glu Glu Glu Glu Asp Glu Glu Glu Asp Asp  
35 40 45

Glu Asp Leu Glu Glu Leu Glu Val Leu Glu Arg Lys Pro Ala Ala Gly  
50 55 60

Leu Ser Ala Ala Ala Val Pro Pro Ala Ala Ala Pro Leu Leu Asp  
65 70 75 80

Phe Ser Ser Asp Ser Val Pro Pro Ala Pro Arg Gly Pro Leu Pro Ala

85

90

95

Ala Pro Pro Ala Ala Pro Glu Arg Gln Pro Ser Trp Glu Arg Ser Pro

100

105

110

Ala Ala Pro Ala Pro Ser Leu Pro Pro Ala Ala Ala Val Leu Pro Ser

115

120

125

Lys Leu Pro Glu Asp Asp Glu Pro Pro Ala Arg Pro Pro Pro Pro Pro

130

135

140

Pro Ala Gly Ala Ser Pro Leu Ala Glu Pro Ala Ala Pro Pro Ser Thr

145

150

155

160

Pro Ala Ala Pro Lys Arg Arg Gly Ser Gly Ser Val Asp Glu Thr Leu

165

170

175

Phe Ala Leu Pro Ala Ala Ser Glu Pro Val Ile Pro Ser Ser Ala Glu

180

185

190

Lys Ile Met Asp Leu Met Glu Gln Pro Gly Asn Thr Val Ser Ser Gly

195

200

205

Gln Glu Asp Phe Pro Ser Val Leu Leu Glu Thr Ala Ala Ser Leu Pro

210

215

220

Ser Leu Ser Pro Leu Ser Thr Val Ser Phe Lys Glu His Gly Tyr Leu  
225 230 235 240

Gly Asn Leu Ser Ala Val Ser Ser Ser Glu Gly Thr Ile Glu Glu Thr  
245 250 255

Leu Asn Glu Ala Ser Lys Glu Leu Pro Glu Arg Ala Thr Asn Pro Phe  
260 265 270

Val Asn Arg Asp Leu Ala Glu Phe Ser Glu Leu Glu Tyr Ser Glu Met  
275 280 285

Gly Ser Ser Phe Lys Gly Ser Pro Lys Gly Glu Ser Ala Ile Leu Val  
290 295 300

Glu Asn Thr Lys Glu Glu Val Ile Val Arg Ser Lys Asp Lys Glu Asp  
305 310 315 320

Leu Val Cys Ser Ala Ala Leu His Ser Pro Gln Glu Ser Pro Val Gly  
325 330 335

Lys Glu Asp Arg Val Val Ser Pro Glu Lys Thr Met Asp Ile Phe Asn  
340 345 350

Glu Met Gln Met Ser Val Val Ala Pro Val Arg Glu Glu Tyr Ala Asp  
355 360 365

Phe Lys Pro Phe Glu Gln Ala Trp Glu Val Lys Asp Thr Tyr Glu Gly

370

375

380

Ser Arg Asp Val Leu Ala Ala Arg Ala Asn Val Glu Ser Lys Val Asp  
385 390 395 400

Arg Lys Cys Leu Glu Asp Ser Leu Glu Gln Lys Ser Leu Gly Lys Asp  
405 410 415

Ser Glu Gly Arg Asn Glu Asp Ala Ser Phe Pro Ser Thr Pro Glu Pro  
420 425 430

Val Lys Asp Ser Ser Arg Ala Tyr Ile Thr Cys Ala Ser Phe Thr Ser  
435 440 445

Ala Thr Glu Ser Thr Thr Ala Asn Thr Phe Pro Leu Leu Glu Asp His  
450 455 460

Thr Ser Glu Asn Lys Thr Asp Glu Lys Lys Ile Glu Glu Arg Lys Ala  
465 470 475 480

Gln Ile Ile Thr Glu Lys Thr Ser Pro Lys Thr Ser Asn Pro Phe Leu  
485 490 495

Val Ala Val Gln Asp Ser Glu Ala Asp Tyr Val Thr Thr Asp Thr Leu  
500 505 510

Ser Lys Val Thr Glu Ala Ala Val Ser Asn Met Pro Glu Gly Leu Thr  
515 520 525

Pro Asp Leu Val Gln Glu Ala Cys Glu Ser Glu Leu Asn Glu Ala Thr  
530 535 540

Gly Thr Lys Ile Ala Tyr Glu Thr Lys Val Asp Leu Val Gln Thr Ser  
545 550 555 560

Glu Ala Ile Gln Glu Ser Leu Tyr Pro Thr Ala Gln Leu Cys Pro Ser  
565 570 575

Phe Glu Glu Ala Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val  
580 585 590

Met Glu Ala Pro Leu Asn Ser Leu Leu Pro Ser Ala Gly Ala Ser Val  
595 600 605

Val Gln Pro Ser Val Ser Pro Leu Glu Ala Pro Pro Pro Val Ser Tyr  
610 615 620

Asp Ser Ile Lys Leu Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu Ala  
625 630 635 640

Met Asn Val Ala Leu Lys Ala Leu Gly Thr Lys Glu Gly Ile Lys Glu  
645 650 655

Pro Glu Ser Phe Asn Ala Ala Val Gln Glu Thr Glu Ala Pro Tyr Ile  
660 665 670

Ser Ile Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser Thr Glu Pro

675

680

685

Ser Pro Asp Phe Ser Asn Tyr Ser Glu Ile Ala Lys Phe Glu Lys Ser

690

695

700

Val Pro Glu His Ala Glu Leu Val Glu Asp Ser Ser Pro Glu Ser Glu

705

710

715

720

Pro Val Asp Leu Phe Ser Asp Asp Ser Ile Pro Glu Val Pro Gln Thr

725

730

735

Gln Glu Glu Ala Val Met Leu Met Lys Glu Ser Leu Thr Glu Val Ser

740

745

750

Glu Thr Val Ala Gln His Lys Glu Glu Arg Leu Ser Ala Ser Pro Gln

755

760

765

Glu Leu Gly Lys Pro Tyr Leu Glu Ser Phe Gln Pro Asn Leu His Ser

770

775

780

Thr Lys Asp Ala Ala Ser Asn Asp Ile Pro Thr Leu Thr Lys Lys Glu

785

790

795

800

Lys Ile Ser Leu Gln Met Glu Glu Phe Asn Thr Ala Ile Tyr Ser Asn

805

810

815

Asp Asp Leu Leu Ser Ser Lys Glu Asp Lys Ile Lys Glu Ser Glu Thr  
820 825 830

Phe Ser Asp Ser Ser Pro Ile Glu Ile Ile Asp Glu Phe Pro Thr Phe  
835 840 845

Val Ser Ala Lys Asp Asp Ser Pro Lys Leu Ala Lys Glu Tyr Thr Asp  
850 855 860

Leu Glu Val Ser Asp Lys Ser Glu Ile Ala Asn Ile Gln Ser Gly Ala  
865 870 875 880

Asp Ser Leu Pro Cys Leu Glu Leu Pro Cys Asp Leu Ser Phe Lys Asn  
885 890 895

Ile Tyr Pro Lys Asp Glu Val His Val Ser Asp Glu Phe Ser Glu Asn  
900 905 910

Arg Ser Ser Val Ser Lys Ala Ser Ile Ser Pro Ser Asn Val Ser Ala  
915 920 925

Leu Glu Pro Gln Thr Glu Met Gly Ser Ile Val Lys Ser Lys Ser Leu  
930 935 940

Thr Lys Glu Ala Glu Lys Lys Leu Pro Ser Asp Thr Glu Lys Glu Asp  
945 950 955 960

Arg Ser Leu Ser Ala Val Leu Ser Ala Glu Leu Ser Lys Thr Ser Val

965

970

975

Val Asp Leu Leu Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val Val Phe  
980 985 990

Gly Ala Ser Leu Phe Leu Leu Leu Ser Leu Thr Val Phe Ser Ile Val  
995 1000 1005

Ser Val Thr Ala Tyr Ile Ala Leu Ala Leu Leu Ser Val Thr Ile  
1010 1015 1020

Ser Phe Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile Gln Lys Ser  
1025 1030 1035

Asp Glu Gly His Pro Phe Arg Ala Tyr Leu Glu Ser Glu Val Ala  
1040 1045 1050

Ile Ser Glu Glu Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly  
1055 1060 1065

His Val Asn Ser Thr Ile Lys Glu Leu Arg Arg Leu Phe Leu Val  
1070 1075 1080

Asp Asp Leu Val Asp Ser Leu Lys Phe Ala Val Leu Met Trp Val  
1085 1090 1095

Phe Thr Tyr Val Gly Ala Leu Phe Asn Gly Leu Thr Leu Leu Ile  
1100 1105 1110

Leu Ala Leu Ile Ser Leu Phe Ser Ile Pro Val Ile Tyr Glu Arg  
1115 1120 1125

His Gln Val Gln Ile Asp His Tyr Leu Gly Leu Ala Asn Lys Ser  
1130 1135 1140

Val Lys Asp Ala Met Ala Lys Ile Gln Ala Lys Ile Pro Gly Leu  
1145 1150 1155

Lys Arg Lys Ala Asp  
1160

<210> 27

<211> 25

<212> PRT

<213> *Rattus norvegicus*

<220>

<221> PEPTIDE

<222> (1) .. (25)

<223> rat PEP4

<400> 27

Glu Glu Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly His Val Asn  
1 5 10 15

Ser Thr Ile Lys Glu Leu Arg Arg Leu  
20 25

<210> 28

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> PRO/SER rich peptide

<220>

<221> PEPTIDE

<222> (1)..(17)

<223> Synthetic peptide

<400> 28

Pro Ser Ser Pro Pro Pro Ser Ser Pro Pro Pro Pro Ser Ser Pro Pro Pro

1 5 10 15

Ser

<210> 29

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> CA-NA-2F

<220>

<221> primer\_bind

<222> (1) .. (25)

<223> CA-NA-2F primer

<400> 29

aagcaccatt gaattctgca gttcc

<210> 30

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> CA-NA-3R

<220>

<221> primer\_bind

<222> (1)..(28)

<223>

<400> 30

aactgcagta ctgagctcct ccatctgc

28

<210> 31

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> forward 5'

<220>

<221> primer\_bind

<222> (1)..(33)

<223> forward primer

<400> 31

gtcgcggatc catggagacc ctttttgctc ttc

33

<210> 32

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> reverse 5'

<220>

<221> primer\_bind

<222> (1) .. (27)

<223> reverse primer

<400> 32

tttctcgagt tatgaagttt tactcag

27

<210> 33

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> forward 5'-1

<220>

<221> primer\_bind

<222> (1) .. (29)

<223> primer

<400> 33

gtgcggatcc atggatttga aggagcagc

29

<210> 34

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> reverse 5'-1

<220>

<221> primer\_bind

<222> (1)..(28)

<223> primer

<400> 34

gtttctcgag tgaagttta ttcagctc

28

<210> 35

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' primer

<220>

<221> primer\_bind

<222> (1) .. (20)

<223> primer

<400> 35

tccaccccg<sub>1</sub> ccgcgc<sub>2</sub> ccaa

20

<210> 36

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' primer 2

<220>

<221> primer\_bind

<222> (1) .. (22)

<223> primer

<400> 36

aatgatgggc aaagctgtgc tg

22

<210> 37

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> 3' primer

<220>

<221> primer\_bind

<222> (1) .. (24)

<223> primer

<400> 37

ggtacaaaaga ttgcttatga aaca

24

<210> 38

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> 3' primer 2

<220>

<221> primer\_bind

<222> (1) .. (22)

<223> primer

<400> 38

agcagggcca aggcaatgtt gg

22

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> 5'-VL leader

<220>

<221> primer\_bind

<222> (1)..(28)

<223> primer

<400> 39

aatatgagtc ctgccccagtt cctgtttc

28

<210> 40

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> 3'-Ck

<220>

<221> primer\_bind

<222> (1)..(32)

<223> primer

<400> 40

ttaggaattc ctaacactct cccctgttga ag

32

<210> 41

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> 5'-VH leader

<220>

...

<222> (1) .. (31)

<223> primer

<400> 41

aatatggatt ttgggctgat ttttttatt g

31

<210> 42

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> 3'-CH hinge

<220>

<221> primer\_bind

<222> (1) .. (24)

<223> primer

<400> 42

aattgggcaa cgttgcaggt gacg

24

<210> 43

<211> 663

<212> DNA

<213> *Mus musculus*

<220>

<221> misc\_binding

<222> (1)..(663)

<223> DNA variable part of heavy chain 11C7

<400> 43

atggattttg ggctgatttt ttttattgtt ggtcttttaa aaggggtcca gtgtgaggtg 60

aagcttctcg agtctggagg tggcctggtg cagcctggag gatccctgaa actctcctgt 120

gtagtctcag gattcgattt tagaagaaat tggatgagtt gggtcggca ggctcctgg 180

aaagggctag aatggattgg agaaattaat ccagatagca gtaagataaa ctatacgcca 240

tctctaaagg ataaattcat catctccaga gacaatgcc agaatacgct gtacctgcaa 300

gtgagcacag tgagatctga ggacacagcc ctttattact gtgtgagacc ggtctggatg 360

tatgctatgg actactgggg tcaaggaacc tcagtcaccg tctcctcagc caaaaacgaca 420

cccccatctg tctatccact ggccctgga tctgctgcc aaactaactc catggtgacc 480

ctgggatgcc tggtaaggg ctatccct gagccagtga cagtgacctg gaactctgga	540
tccctgtcca gcggtgtgca caccccca gctgtcctgc agtctgacct ctacactctg	600
agcagctcag tgactgtccc ctccagcacc tggccagcg agaccgtcac ctgcaacgtt	660
gcc	663

<210> 44

<211> 717

<212> DNA

<213> *Mus musculus*

<220>

<221> misc\_binding

<222> (1) .. (717)

<223> variable part of light chain of 11C7

<400> 44

atgagtccctg cccagttcct gtttctgtta gtgctctgga ttccggaaac cagcgggtat	60
--	----

gttctgttga cccagactcc tctcactttg tcgataacca ttggacaaacc agcctccatc	120
--	-----

tcttgcaagt caagtcagag cctcttgcattt agtgcattttt gaattgggtt	180
---	-----

ttacagaggc caggccagtc tccaaagcgc ctaatctatc tggtgtctaa actggactct 240  
ggagtcctcg acaggttcac tggcagtgga tcagggacgg atttcacact gaaaatcagc 300  
agagtggagg ctgaggattt gggactttat tattgctggc aaggtacaca ttttcctcag 360  
acgttcggtg gaggcaccaa gctggaaatc aaacgggctg atgctgcacc aactgtatcc 420  
atcttcccac catccagtga gcagtttaca tctggagggtg cctcagtcgt gtgcttcttg 480  
aacaacttct accccaaaga catcaatgtc aagtggaaaga ttgatggcag tgaacgacaa 540  
aatggcgtcc tgaacagttg gactgatcag gacagcaaag acagcaccta cagcatgagc 600  
agcaccctca cgttgaccaa ggacgagttt gaacgacata acagctatac ctgtgaggcc 660  
actcacaaga catcaacttc acccattgtc aagagcttca acaggggaga gtgttag 717